| Edited and Edited the Added the Edited the Changed Corrected Corre | Ithe margins in cases where the sequence text was "wrapp format error in the Current Application Data section, specific a Current Application Data section with the actual current news the prior application data; or other amandatory heading and subheadings for "Current Application of Sequences" field. The applicant spelled out a the spelling of a mandatory field (the headings or subheading the SEQ ID NO when obviously incorrect. The sequence of the corrected a nucleic number at the end of a nucleic line. Sequenced to subheading placement. All responses must be on the same | cally: umber. The number inputted by the tion Data". number instead of using an integer and integer |
|--|---|---|
| Edited and Edited the Edited the Changed Corrected Corre | format error in the Current Application Data section, specific a Current Application Data section with the actual current news the prior application data; or other amandatory heading and subheadings for "Current Applica" Number of Sequences" field. The applicant spelled out a the spelling of a mandatory field (the headings or subheading the SEQ ID NO when obviously incorrect. The sequence of a corrected a nucleic number at the end of a nucleic line. Subheading placement. All responses must be on the same | ed" down to the next line. cally: umber. The number inputted by the tion Data". number instead of using an integer ngs), specifically: numbers that were edited were: |
| Edited the applicant Added the Edited the Changed Corrected Correc | e Current Application Data section with the actual current news the prior application data; or other mandatory heading and subheadings for "Current Application data; or "Number of Sequences" field. The applicant spelled out a the spelling of a mandatory field (the headings or subheading the SEQ ID NO when obviously incorrect. The sequence of the corrected a nucleic number at the end of a nucleic line. Sequenced to subheading placement. All responses must be on the same | tion Data*. number instead of using an integer ngs), specifically: numbers that were edited were: |
| Added the Edited the Changed Corrected Correct | was the prior application data; or other mandatory heading and subheadings for "Current Applica "Number of Sequences" field. The applicant spelled out a the spelling of a mandatory field (the headings or subheading the SEQ ID NO when obviously incorrect. The sequence of corrected a nucleic number at the end of a nucleic line. Subheading placement. All responses must be on the same | tion Data*. number instead of using an integerings), specifically: numbers that were edited were: |
| Corrected | e "Number of Sequences" field. The applicant spelled out a the spelling of a mandatory field (the headings or subheading the SEQ ID NO when obviously incorrect. The sequence of a corrected a nucleic number at the end of a nucleic line. Subheading placement. All responses must be on the same | number instead of using an integerings), specifically: numbers that were edited were: |
| Changed Corrected Inserted of | the spelling of a mandatory field (the headings or subheading the SEQ ID NO when obviously incorrect. The sequence of a corrected a nucleic number at the end of a nucleic line. Subheading placement. All responses must be on the same | ngs), specifically: numbers that were edited were: EQ ID NO's edited: |
| Corrected Corrected | the SEQ ID NO when obviously incorrect. The sequence of corrected a nucleic number at the end of a nucleic line. Subheading placement. All responses must be on the same | numbers that were edited were: |
| Inserted of | the SEQ ID NO when obviously incorrect. The sequence of a nucleic number at the end of a nucleic line. Subheading placement. All responses must be on the same | numbers that were edited were: |
| Corrected | subheading placement. All responses must be on the same | |
| | | |
| | placed a response below the subheading, this was moved to | |
| Inserted o | olons after headings/subheadings. Headings edited include | ed: |
| Deleted a | dra, invalid, headings used by an applicant, specifically: | |
| | ☐ non-ASCII "garbage" at the beginning/end of files; ☐ s numbers throughout text; ☐ other invalid text, such as | |
| Inserted i | nandatory headings, specifically: | |
| | an obvious error in the response, specifically: | unius. |
| Edited ide | ntifiers where upper case is used but lower case is required | • |
| . Corrected | an error in the Number of Sequences field, specifically: | |
| A "Hard P | age Break* code was inserted by the applicant. All occurren | ices had to be deleted. |
| Deleted end | fling stop codon in amino acid sequences and adjusted the entIn bug). Sequences corrected: | *(A)Length:* field accordingly (erro |
| Other: | | |

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.



OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/099,830B

DATE: 12/12/2002
TIME: 17:47:21

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\12122002\J099830B.raw

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              Knox, Richard John
      8 <120> TITLE OF INVENTION: Therapeutic Systems
     10 <130> FILE REFERENCE: ERD 100 CON
     12 <140> CURRENT APPLICATION NUMBER: 10/099,830B
     13 <141> CURRENT FILING DATE: 2002-03-13
     15 <150> PRIOR APPLICATION NUMBER: 09/445,865
     16 <151> PRIOR FILING DATE: 2000-02-11
     18 <160> NUMBER OF SEQ ID NOS: 2
     20 <170> SOFTWARE: PatentIn version 3.1
     22 <210> SEQ ID NO: 1
     23 <211> LENGTH: 24
     24 <212> TYPE: DNA
     25 <213> ORGANISM: Artificial Sequence
     28 <220> FEATURE:
     29 <223> OTHER INFORMATION: nucleotide incorporating XhoI, Kozak sequence, and NcoI site
     31 <220> FEATURE:
     32 <221> NAME/KEY: misc feature
     33 <222> LOCATION: (22) 7. (24)
     34 <223> OTHER INFORMATION: n at positions 22, 23 and 24 can be any nucleotide
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W-39 cctcgagtca ccatggatat cnnn
                                                                                24
     42 <210> SEO ID NO: 2
     43 <211> LENGTH: 697
     44 <212> TYPE: DNA
     45 <213> ORGANISM: Homo sapiens
     49 <220> FEATURE:
     50 <221> NAME/KEY: misc feature
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                                                                               120
     60 gatttgtatg ccatgaactt tgagccgagg gccacagaca aagatatcac tggtactctt
                                                                               180
                                                                               240
     62 totaatootg aggttttcaa ttatggagtg gaaacccacg aagcctacaa gcaaaggtct
                                                                               300
     64 ctqqctaqcq acatcactqa tqaqcaqaaa aaqqttcqqa qqctqaccta qtqatatttc
     66 agttcccqct qtactqqttc aqcqtqccqq ccatcctgaa qqqctqqatq gataqqqtqc
                                                                               360
     68 tgtgccaqqg ctttgccttt qacatcccag gattctacga ttccggtttg ctccagggta
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     72 tcaatggaga ttctcgatac ttcctgtggc cactccagca tggcacatta cacttctgtg
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     74 gatttaaagt ccttgcccct cagatcagct ttgctcctga aattgcatcc gaagaagaaa
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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/099,830B

DATE: 12/12/2002
TIME: 17:47:22

Output Set: N:\CRF4\12122002\J099830B.raw

Input Set : A:\PTO.AMC.txt

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 22,23,24